

Sequence Listing

<110> Kaneka Corporation

<120> NOVEL CARBONYL REDUCTASE, GENE THEREFOR, AND METHOD OF USING THE SAME

<130> T609HOP-GT

<150> JP2000-232756

<151> 2000-08-01

<160> 11

<210> 1

<211> 277

<212> PRT

<213> Micrococcus luteus

<400> 1

Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly

1 5 10 15

Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu

20 25 30

Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp

35 40 45

Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu

50 55 60

Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met

65 70 75 80

Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser

85 90 95

Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu Leu His Trp

100 105 110

Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu

115 120 125

Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His

130 135 140

Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr

145 150 155 160

Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp

165 170 175

Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser

180 185 190

Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val

195 200 205

Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Leu Ala Trp Val

210 215 220

Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln

225 230 235 240

His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu

245 250 255

Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg

260 265 270

Pro Leu Glu Met Leu

275

<210> 2

<211> 834

<212> DNA

<213> Micrococcus luteus

<400> 2

atg cga cgg atg acg ctg ccg agt ggg gag tcc atc cct gtg ctg ggc
 Met Arg Arg Met Thr Leu Pro Ser Gly Glu Ser Ile Pro Val Leu Gly

1 5 10 15

cag ggc acc tgg ggc tgg ggt gag gac ccc ggc cgc cgc ggc gac gag
 Gln Gly Thr Trp Gly Trp Gly Glu Asp Pro Gly Arg Arg Gly Asp Glu

20 25 30

gtc gcc gcg ctg cac gcc ggc ctc gag ctg ggc atg acg ctg gtc gac
 Val Ala Ala Leu His Ala Gly Leu Glu Leu Gly Met Thr Leu Val Asp

35 40 45

acc gcc gag atg tac gcc gac ggc ggt gcg gag gag gtg gct ggt gaa
 Thr Ala Glu Met Tyr Ala Asp Gly Gly Ala Glu Glu Val Ala Gly Glu

50 55 60

gca ttg gcg ggt cgc cgc gac gag gcg ttc gtg gtc agc aag gtc atg
 Ala Leu Ala Gly Arg Arg Asp Glu Ala Phe Val Val Ser Lys Val Met

65 70 75 80

ccg tcc cac gcc tcc cgt tcc ggc acg atc gcg gcc tgc gaa cgc agc
 Pro Ser His Ala Ser Arg Ser Gly Thr Ile Ala Ala Cys Glu Arg Ser

85 90 95

ctg aaa cgc ctg ggc acc gat cgg atc gac ctc tac ctg ctg cac tgg
 Leu Lys Arg Leu Gly Thr Asp Arg Ile Asp Leu Tyr Leu His Trp

100 105 110

cag ggc agg tac ccg ctg cag gac acc gtc gcg gcc ttc cac cag ctc
 Gln Gly Arg Tyr Pro Leu Gln Asp Thr Val Ala Ala Phe His Gln Leu

115 120 125

gtc gag gac ggg aaa atc cga tac tgg ggc gtc agc aac ttc gac cac
 Val Glu Asp Gly Lys Ile Arg Tyr Trp Gly Val Ser Asn Phe Asp His

130 135 140

cg^g gc^c ct^c gc^c ga^g ct^g ca^g ga^c gt^g cc^g gc^c ac^c ag^c gg^g ct^g ac^c
 Arg Ala Leu Ala Glu Leu Gln Asp Val Pro Gly Thr Ser Gly Leu Thr
 145 150 155 160

ac^g ga^t ca^g gt^g ct^g ta^c a^a ct^g tc^g cg^g ca^g gg^a cc^g ga^g ta^c ga^c
 Thr Asp Gln Val Leu Tyr Asn Leu Ser Arg Arg Gly Pro Glu Tyr Asp
 165 170 175

ct^g ct^g cc^g tg^g tg^c gc^c ga^c ca^c ca^g ct^g cc^g gt^c at^g gc^g ta^c tc^g
 Leu Leu Pro Trp Cys Ala Asp His Gln Leu Pro Val Met Ala Tyr Ser
 180 185 190

cc^g at^c ga^g ca^g gg^c cg^c at^c ct^t ga^c ac^g ac^g ct^g a^a gc^c gt^c
 Pro Ile Glu Gln Gly Arg Ile Leu Asp Asp Thr Thr Leu Asn Asp Val
 195 200 205

gc^g gc^c cg^t ca^c ag^c gt^c ag^c cc^c gc^g gc^g gc^g cc^c tt^t gc^c tg^g gt^g
 Ala Ala Arg His Ser Val Ser Pro Ala Ala Ala Leu Ala Trp Val
 210 215 220

ct^g cg^c cg^c ga^c tc^g ct^c tg^c ac^g at^c cc^c a^a g^g gc^g ag^c ag^c cc^g ca^g
 Leu Arg Arg Asp Ser Leu Cys Thr Ile Pro Lys Ala Ser Ser Pro Gln
 225 230 235 240

ca^c gt^g cg^c ga^c a^a gc^c a^c a^g ct^g ga^c gt^g ga^g ct^g ac^c cg^c ga^a
 His Val Arg Asp Asn Ala Thr Ala Leu Asp Val Glu Leu Thr Arg Glu
 245 250 255

ga^c ct^g ga^t g^c t^t g^c ct^g ga^c cg^t tt^t cc^c cc^c cc^g ag^c gg^a cc^g cg^a
 Asp Leu Asp Ala Leu Asp Arg Ala Phe Pro Pro Pro Ser Gly Pro Arg
 260 265 270

cc^a ct^g ga^a at^g ct^g t^ga
 Pro Leu Glu Met Leu
 275

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 3

gayacngcng aratgtaygc

20

<210> 4

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 4

tctytenacna gytgrtgaa

20

<210> 5

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 5

gctgcatatgc gacggatgac gctgcc

26

<210> 6

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 6

ggcgaattct tacagcattt ccagtggtcg cg

32

<210> 7

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 7

gcgaattcta aggagattt aatatgcac ggatgacgct gcccag

46

<210> 8

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 8

caggagctct tacagcattt ccagtggtc

29

<210> 9

<211> 144

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: double-stranded DNA

<400> 9

gaattctaag gagatttaca tatgcgttgt atgactttac catctggtga atctattcca

60

gttttaggtc aaggtacttg gggttgggtt gaagatccag gtcgttgtgg tcatgaagtt

120

gctgcttac atgctggct cgag

<210> 10

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 10

caggagctct aaggaggta acaatgtata aag 33

<210> 11

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

cacggatcct tatecgctc ctgcttgg 28